

LOCUS	COMMON	ACCESSION	LENGTH	REGION	FIRST AUTHOR	REFERENCE
HIVU53175	HIVCA9	U53175	422 bp	gag	Braaten, D.	JVI 70, 4220 (1996)
Comment: This study compared the five lineages of primate immunodeficiency viruses and found that only HIV-1 group M requires cyclophilin A for replication. HIV-1 gag binds to cyclophilin A and incorporates it into virions. If this process is disrupted, virion infectivity is inhibited. Cloned isolates from clades A, B, and D of HIV-1 group M and two clones from group O were used. This first phenotypic difference between group M and group O is consistent with the idea that the two HIV-1 groups were introduced to humans by different zoonotic transmissions. This sequence was obtained by PCR from human PBMCs infected with HIVCA9, a group O virus from Cameroon. GenBank accession number U53175.						
HIVU54771	CM240	U54771	9203 bp	comp. gen.	Carr, J.K.	JVI 70, 5935 (1996)
Comment: Blood from an asymptomatic heterosexual 21-year-old Thai man was transported from Thailand to the USA where PBMCs were separated and co-cultivated with PHA-stimulated donor PBMCs. DNA from p24 antigen-positive culture was used to amplify the proviral DNA. The complete genomic sequence of the provirus was determined by the compilation of three clones containing different parts of the viral genome. CM240 is an example of a Thai subtype E virus, which is a mosaic of a clade A virus and a clade E virus. GenBank accession number U54771.						
SIU17646	SIVsmSL92a	U17646	825 bp	gag	Chen, Z.	JVI 70, 3617 (1996)
Comment: Eight SIV gag and env sequences from sooty mangabeys. Six of them represent new viruses from West Africa. All belonged to the SIVsm/HIV-2 family. The characterization of these sequences supports the hypothesis that each HIV-2 subtype in West Africans originated from widely divergent SIVsm strains, transmitted by independent cross-species events in the same geographic locations. GenBank accession numbers U17646,U48810-U48824.						
HIVU52194		U52194	325 bp	gag	Diaz, R.S.	Unpublished (1996)
Comment: This work also includes ten envelope sequences. GenBank accession numbers U52194 and U51942,U52055-U52603.						
HIVU56888	1C	U56888	402 bp	gag	Fultz, P.N.	Unpublished (1996)
Comment: A set of 12 gag sequences and 12 env sequences from a study on the diversification of two HIV-1 LAI Subtype B strains during the dual infection of a chimpanzee for nine years. GenBank accession numbers U56866-U56899.						
HIVU51188	90CR402	U51188	9843 bp	comp. gen.	Gao, F.	JVI 70, 7013 (1996)
Comment: One of a set of three complete genomes from a study linking the HIV-1 epidemic in the heterosexual population in Thailand to an A/E recombinant. 90CR402, previously named CAR-E 4002, was obtained from a man from Bangui, Central African Republic, who had lymphadeopathy, diarrhea, severe weight loss and recurrent respiratory infections. He was infected through heterosexual contact, but the year of infection is unknown. 90CR402 (U51188) was first adapted to growth in chimpanze cells, expanded in chimpanzee cells, and then re-expanded in human PBMCs before lambda cloning and sequencing. 93TH253 (U51189) is from a 21-year-old man from Chiang Mai, Thailand and was previously named CMU010 or 302053. The patient had end-stage AIDS. The mode and year of infection are unknown. 93TH253 was isolated and expanded in human PBMCs, then expanded in H9 cells followed by lambda cloning and sequencing. 92UG037 (U51190) was obtained from WHO-NIAIDS and comes from an asymptomatic 31-year-old female from Entebbe, Uganda, early in infection. The year of infection is unknown and the mode of infection was heterosexual contact. 92UG037 was established and propagated by cocultivation with normal donor lymphocytes, and then PCR amplified and sequenced. 93TH253 and 90CR402 are subtype E (A/E recombinant). Comparison of the two strains showed that they were derived from a common A/E recombinant ancestor, presumably from Central Africa. 92UG037 is subtype A. LTR sequences are available under accession numbers U51282-U51297.						
SIVCPZANT	CPZANT	U42720	8182 bp	comp. gen.	Vanden Haesevelde, M.	Virology 221, 346 (1996)
Comment: A simian immunodeficiency virus phylogenetically linked to HIV-1 which was isolated from a captured wild chimpanzee from Zaire. This is the third SIV strain linked to HIV-1 after SIVCPZ-GAB (X52154) and SIVCPZ-GAB2 (U11495) isolated from chimps in Gabon. While SIVCPZ-ANT and SIVCPZ-GAB share a common ancestor with HIV-1, they differ in that the SIVCPZ strains have highly conserved V3 regions and HIV-1 has a highly variable V3 region. SIVCPZ-ANT is considered to be an outgroup of HIV-1 and is used to suggest the possibility of various introductions of HIV-1 into the human population.						
HO74C12DG	074	Z76649	390 bp	gag	Kampinga, G.A.	Unpublished (1996)
Comment: A set of 224 sequences from an extensive HIV-1 mother-to-child-transmission study in Rwanda. The study covers heterogeneity and coinfection with subtypes A and C. GenBank accession numbers Z75969-Z75978, Z75989-Z75997, Z76010-Z76019, Z76030-Z76038, Z76043, Z76045, Z76047, Z76058-Z76069, Z76071-Z76073, Z76084-Z76093, Z76104-Z76113, Z76123-Z76133, Z76144-Z76152, Z76154-Z76159, Z76162-Z76166, Z76177-Z76182, Z76184-Z76187, Z76208-Z76217, Z76232, Z76246, Z76249-Z76261, Z76274, Z76283, Z76294, Z76302, Z76312-Z76321, Z76343-Z76352, Z76363-Z76372, Z76383-Z76392, Z76413-Z76422, Z76433-Z76442, Z76453-Z76462, Z76649, Z76706, Z76707, Z76733.						

## HIV-1 GAG Sequence Summaries

HIVU70271 LIT9485 U70271 210 bp gag Liitsola, K. J. Infect. Dis. In press (1996)  
 Comment: One of thirty-four Baltic and Russian sequences derived from PCR amplified DNA from PBMCs. GenBank accession numbers U70271-U70304.

HIVMCK1 MCK1 D86068 9752 bp comp. gen. Iwatani, Y. Unpublished (1996)  
 Comment: This sequence is ~98% identical to HXB2 and other IIIB lab strains of HIV-1. PM213 is another complete genome also ~98% identical to HXB2. GenBank accession numbers D86068 and D86069.

HBABMNT BAB-MNT X99948 387 bp gag Narwa, R. JVI 70, 4474 (1996)  
 Comment: A set of 54 sequences from a mother-to-child-transmission study. The encoding regions of the matrix protein, p17, were sequenced from viral isolates from 22 nontransmitting mothers, 12 HIV-1 positive mother-and-child pairs, 4 infected children, and 4 transmitting mothers. All patients were attending urban hospitals in Paris. Blood samples taken during delivery for mothers and the first month of life for infants. Most of the European mothers were drug users or sexual partners of drug users. The main route of infection for African mothers was heterosexual intercourse. Sequences were classified among the A, B and G subtypes. GenBank accession numbers X99948-X99949, Z79527-Z79578.

HIVETH2220 ETH2220 U46016 9031 bp comp. gen. Salminen, M.O. ARHR 12, 1329 (1996)  
 Comment: U46016 is the first reported (almost full length) subtype C sequence from Ethiopia. In its genomic organization, this clone closely resembles subtype A, B, and D isolates except that the core promoter contains three potential binding sites for the transcription factor NF- $\kappa$ B instead of containing two.

HIVKUMM1C KUMM1 L42019 410 bp gag Voevodin, A. ARHR 12, 641 (1996)  
 Comment: Six sequences (I1-5, KUMM2) from Indian expatriates in Kuwait and one sequence from an Ethiopian expatriate in Kuwait used in a study of the diversity of subtypes found in India, Ethiopia, and Kuwait using gag nucleotide sequences. Voevodin et al. found that isolates KUMM1, KUMM2, I1, I3, I4, and I5 clustered with subtype C while the rest clustered with subtype B sequences. GenBank accession numbers U42013, L42014, L42016-L42019, L42022.

LOCUS	COMMON	ACCESSION	LENGTH	REGION	FIRST AUTHOR	REFERENCE
HIVU53606	MB.01	U53606	306 bp	pol (protease)	Barrie, K.A.	Virology 219, 407 (1996)
Comment: This study analyzed HIV-1 gag and pol sequences from PBMCs from HIV-1-infected mothers and their children. Sixty protease alleles from 12 individuals differed by from 3 to as many as 10 amino acids. Protease variants with a proline at position 63, a substitution associated with resistance to protease inhibitors, appeared in the absence of antiprotease therapy in 7 patients and were transmitted by 2 mothers to their infants. Gag p7 p6 regions were more variable than protease. GenBank accession numbers for the set of 61 sequences are U53606-U53666.						
HIVU54771	CM240	U54771	9203 bp	comp. gen.	Carr, J.K.	JVI 70, 5935 (1996)
Comment: Blood from an asymptomatic heterosexual 21-year-old Thai man was transported from Thailand to the USA where PBMCs were separated and co-cultivated with PHA-stimulated donor PBMCs. DNA from p24 antigen-positive culture was used to amplify the proviral DNA. The complete genomic sequence of the provirus was determined by the compilation of three clones containing different parts of the viral genome. CM240 is an example of a Thai subtype E virus, which is a mosaic of a clade A virus and a clade E virus. GenBank accession number U54771.						
HIVU50207	HIVZ321B	U50207	1497 bp	gag, pol	Choi, D.J.	Unpublished (1996)
Comment: The virus HIVZ321B is a later passage of HIVZ321 (GenBank accession number M15896), which was isolated from a 1976 Zairian serum sample. Z321 was grown to industrial scale in a chronically infected T-cell line to manufacture an inactivated, therapeutic HIV-1 immunogen. Z321B was established from this industrial scale stock.						
HIV1U45026	74H9E1.2	U45026	117 bp	pol (rt)	Cleland, A.	JAIDS 12, 6 (1996)
Comment: Sequences of the RT domain of HIV1 from ten plasma and PBMCs samples of two hemophiliac patients. Samples were obtained before, during, and after long-term treatment with ZDV. The appearance of resistance-associated substitutions differed in both patients both in order and timing. The sequences were too short to subtype. GenBank accession numbers U45206-U45664.						
HIVU51188	90CR402	U51188	9843 bp	comp. gen.	Gao, F.	JVI 70, 7013 (1996)
Comment: One of a set of three complete genomes from a study linking the HIV-1 epidemic in the heterosexual population in Thailand to an A/E recombinant. 90CR402, previously named CAR-E 4002, was obtained from a man from Bangui, Central African Republic, who had lymphadeopathy, diarrhea, severe weight loss and recurrent respiratory infections. He was infected through heterosexual contact, but the year of infection is unknown. 90CR402 (U51188) was first adapted to growth in chimpanze cells, expanded in chimpanzee cells, and then re-expanded in human PBMCs before lambda cloning and sequencing. 93TH253 (U51189) is from a 21-year-old man from Chiang Mai, Thailand and was previously named CMU010 or 302053. The patient had end-stage AIDS. The mode and year of infection are unknown. 93TH253 was isolated and expanded in human PBMCs, then expanded in H9 cells followed by lambda cloning and sequencing. 92UG037 (U51190) was obtained from WHO-NIAIDS and comes from an asymptomatic 31-year-old female from Entebbe, Uganda, early in infection. The year of infection is unknown and the mode of infection was heterosexual contact. 92UG037 was established and propagated by cocultivation with normal donor lymphocytes, and then PCR amplified and sequenced. 93TH253 and 90CR402 are subtype E (A/E recombinant). Comparison of the two strains showed that they were derived from a common A/E recombinant ancestor, presumably from Central Africa. 92UG037 is subtype A. LTR sequences are available under accession numbers U51282-U51297.						
SIVCPZANT	CPZANT	U42720	8182 bp	comp. gen.	Vanden Haesevelde, M.	Virology 221, 346 (1996)
Comment: A simian immunodeficiency virus phylogenetically linked to HIV-1 which was isolated from a captured wild chimpanzee from Zaire. This is the third SIV strain linked to HIV-1 after SIVCPZ-GAB (X52154) and SIVCPZ-GAB2 (U11495) isolated from chimps in Gabon. While SIVCPZ-ANT and SIVCPZ-GAB share a common ancestor with HIV-1, they differ in that the SIVCPCZ strains have highly conserved V3 regions and HIV-1 has a highly variable V3 region. SIVCPZ-ANT is considered to be an outgroup of HIV-1 and is used to suggest the possibility of various introductions of HIV-1 into the human population.						
HIVMCK1	MCK1	D86068	9752 bp	comp. gen.	Iwatani, Y.	Unpublished (1996)
Comment: This sequence is ~98% identical to HXB2 and other IIIB lab strains of HIV-1. PM213 is another complete genome also ~98% identical to HXB2. GenBank accession numbers D86068 and D86069.						

## HIV-1 POL Sequence Summaries

HIV759RT01 V759 U14902 204 bp pol Quinones, M.E. ARHR 12, 1117 (1996)

Comment: This study looked at sequences from 81 patients from USA, Venezuela, and Spain who were divided into two groups: those with and those without AZT antiretroviral therapy. Several patients had blood drawn on sequential dates to observe change in sequence over time. Patients came from a variety of risk groups, ages, and health status, and a table of patient data is presented. Envelope gene sequences are also available from some of the patients. Not all 81 sequences reported in this paper were released to the database. GenBank accession numbers U14786-U14903, U16764-U16779 and U40533-U40552. The paper also reports on a new sequence analysis software tool for calculating an "evolutionary index" which is a measure of the evolutionary distance between sequences.

HIVETH2220 ETH2220 U46016 9031 bp comp. gen. Salminen, M.O. ARHR 12, 1329 (1996)

Comment: U46016 is the first reported (almost full length) subtype C sequence from Ethiopia. In its genomic organization, this clone closely resembles subtype A, B, and D isolates except that the core promoter contains three potential binding sites for the transcription factor NF-kB instead of containing two.

HIVU53869 PFA330AZT0.2p25 U53869 969 bp pol Tachedjian, G. Virology 212, 58 (1996)

Comment: This sequence was isolated by passing wild-type HIV1 strain PD in the presence of increasing concentrations of AZT and foscarnet in MT-2 cells. Following 25 passes this strain replicated in the presence of 330 micromolar foscarnet and 0.2 micromolar AZT. This protein has three nonpolymorphic substitutions, LYs70Arg, Val75Ile and Lys219Arg, which together give reduced susceptibility to PFA and wild type susceptibility to AZT. The two other sequences in this set also have mutations which give them similar susceptibilities to PFA and AZT. GenBank accession numbers U53669, U53870, and U53871.

SIU65787 SIVmac79A6.1 U65787 1317 bp pol (rt) VanRompay, K.K.A. Unpublished (1996)

Comment: This sequence was derived from an isolate from a rhesus macaque infected with uncloned SIVmac251 following prolonged zidovudine treatment.

HIVU68783 CFSR1 U68783 380 bp pol Wong, J.K. Unpublished (1996)

Comment: Set of 314 sequences of four patients (A, B, C, and D) from San Diego, USA. Samples obtained from the lymph node, spleen, brain, and cerebral spinal fluid of the patients. Sequences are likely from subtype B viruses. GenBank accession numbers for patient A, U68783-U68866; patient B, U68867-U68924; patient C, U68925-U69008; patient D, U69009-U69096.

HIV1AA201 AA201 U64106 738 bp pol (rt) Zheng, N.N. ARHR 12, 1731 (1996)

Comment: Sequences of 91 subtype B HIV-1 isolates obtained between 1990 and 1995 from 23 males from the Sydney region of New South Wales, Australia. These patients were symptomatic or had AIDS, were on long-term antiviral therapy (ZDV and ddI) and showed the development of resistance mutations. Proviral DNA was isolated from PBMCs and the RT region amplified by nested PCR. GenBank accession numbers U64106-U64196.

## HIV-1 Central Region Sequence Summaries

LOCUS	COMMON	ACCESSION	LENGTH	REGION	FIRST AUTHOR	REFERENCE
HIVU54771	CM240	U54771	9203 bp	comp. gen.	Carr, J.K.	JVI 70, 5935 (1996)
Comment: Blood from an asymptomatic heterosexual 21-year-old Thai man was transported from Thailand to the USA where PBMCs were separated and co-cultivated with PHA-stimulated donor PBMCs. DNA from p24 antigen-positive culture was used to amplify the proviral DNA. The complete genomic sequence of the provirus was determined by the compilation of three clones containing different parts of the viral genome. CM240 is an example of a Thai subtype E virus, which is a mosaic of a clade A virus and a clade E virus. GenBank accession number U54771.						
HIVU51188	90CR402	U51188	9843 bp	comp. gen.	Gao, F.	JVI 70, 7013 (1996)
Comment: One of a set of three complete genomes from a study linking the HIV-1 epidemic in the heterosexual population in Thailand to an A/E recombinant. 90CR402, previously named CAR-E 4002, was obtained from a man from Bangui, Central African Republic, who had lymphadenopathy, diarrhea, severe weight loss and recurrent respiratory infections. He was infected through heterosexual contact, but the year of infection is unknown. 90CR402 (U51188) was first adapted to growth in chimpanzee cells, expanded in chimpanzee cells, and then re-expanded in human PBMCs before lambda cloning and sequencing. 93TH253 (U51189) is from a 21-year-old man from Chiang Mai, Thailand and was previously named CMU010 or 302053. The patient had end-stage AIDS. The mode and year of infection are unknown. 93TH253 was isolated and expanded in human PBMCs, then expanded in H9 cells followed by lambda cloning and sequencing. 92UG037 (U51190) was obtained from WHO-NIAIDS and comes from an asymptomatic 31-year-old female from Entebbe, Uganda, early in infection. The year of infection is unknown and the mode of infection was heterosexual contact. 92UG037 was established and propagated by cocultivation with normal donor lymphocytes, and then PCR amplified and sequenced. 93TH253 and 90CR402 are subtype E (A/E recombinant). Comparison of the two strains showed that they were derived from a common A/E recombinant ancestor, presumably from Central Africa. 92UG037 is subtype A. LTR sequences are available under accession numbers U51282-U51297.						
SIVCPZANT	CPZANT	U42720	8182 bp	comp. gen.	Vanden Haesevelde, M.	Virology 221, 346 (1996)
Comment: A simian immunodeficiency virus phylogenetically linked to HIV-1 which was isolated from a captured wild chimpanzee from Zaire. This is the third SIV strain linked to HIV-1 after SIVCPZ-GAB (X52154) and SIVCPZ-GAB2 (U11495) isolated from chimps in Gabon. While SIVCPZ-ANT and SIVCPZ-GAB share a common ancestor with HIV-1, they differ in that the SIVCPZ strains have highly conserved V3 regions and HIV-1 has a highly variable V3 region. SIVCPZ-ANT is considered to be an outgroup of HIV-1 and is used to suggest the possibility of various introductions of HIV-1 into the human population.						
HIVU63314	HIV-1MN	U63314	275 bp	rev	Hua, J.	Virology In press (1996)
Comment: A sequence of HIV-1 MN env and rev genes from a study on the changes of function resulting from a natural sequence variation in the activation domain of HIV-1 rev. GenBank accession number U63314.						
HIVMCK1	MCK1	D86068	9752 bp	comp. gen.	Iwatani, Y.	Unpublished (1996)
Comment: This sequence is ~98% identical to HXB2 and other IIIB lab strains of HIV-1. PM213 is another complete genome also ~98% identical to HXB2. GenBank accession numbers D86068 and D86069.						
HIVU57217	T01	U57217	216 bp	tat	Lorenzo, E.	Unpublished (1996)
Comment: A set of 113 env sequences and 88 tat sequences from US patients derived during a study on the variability of tat and env genes in HIV-1. Sequences are subtype B. GenBank accession numbers U57217-U57304 and U57104-U57216 for the env sequences.						
HIVETH2220	ETH2220	U46016	9031 bp	comp. gen.	Salminen, M.O.	ARHR 12, 1329 (1996)
Comment: U46016 is the first reported (almost full length) subtype C sequence from Ethiopia. In its genomic organization, this clone closely resembles subtype A, B, and D isolates except that the core promoter contains three potential binding sites for the transcription factor NF-kB instead of containing two.						

## HIV-1 ENV Sequence Summaries

LOCUS	COMMON	ACCESSION	LENGTH	REGION	FIRST AUTHOR	REFERENCE
HIVCI17D1	CI17D1	U59559	326 bp	env	Audoly, G.	ARHR In press (1996)
Comment: These sequences are from six different AIDS patients suffering from pulmonary tuberculosis at the Pneumology Hospital of Cocody, Abidjan, Ivory Coast. In this study sequences from viral RNA cocultured on donor PBMCs, proviral DNA sequences from each patients' PBMCs after coculture with donor PBMCs, and proviral DNA sequences directly from uncultured PBMCs were determined. For the cocultured samples viral RNA was harvested from the culture supernatant. PCR or RT-PCR was used to amplify the env V3 region, and 4-7 cloned PCR products were sequenced. A total of 66 sequences from the six patients were published. All 66 were subtype A, and intrapatient sequences were more similar than interpatient sequences. GenBank accession numbers U59559-U59624.						
HIVU46206	BHGM5	U46206	290 bp	env (C2V3)	Barbosa, E.F.	Unpublished (1996)
Comment: Set of three Brazilian sequences. Sequence U46206 was obtained by PCR amplification from DNA derived from PBMCs of a female blood donor of unknown health status. This sample was classified as subtype F by the HMA method. Sequence U46210 was obtained from a male individual of unknown health status and was also classified as subtype F by the HMA method. A third sequence, U46122, was classified as subtype B.						
HIVIU08355	RU103A	U08355	675 bp	env (V3-V5)	Bobkov, A.F.	ARHR 12, 251 (1996)
Comment: One of a set of sequences derived from proviral DNA extracted from PBMCs of a Russian patient. V3-V5 region of env gene extended by nested PCR amplification. The patient belonged to a group of 22 seropositive patients infected nosocomially by HIV-1 originating from a single source. RU103A has a V3 sequence identical to 12 other patients in the group. GenBank accession numbers U08355-U08368.						
HIV1BUK3A	BUK3A	U33095	1089 bp	env (V1-V5)	Bobkov, A.F.	ARHR 12, 1385 (1996)
Comment: Sequences from a study on the genetic variability of HIV-1 in the former Soviet Union. U33095 and U33096 come from a blood sample taken November 1992 from a 39-year-old male Caucasian heterosexual (patient BUK) who lived in Uzbekistan. He reported living in Mozambique in 1984-85 where he was admitted to the hospital several times; however, he reported no sexual relationships with the African residents. Proviral DNA extracted from PBMCs; env gene extended by nested PCR amplification. BUK3A (U33095) and BUK4A (U33096) belong to subtype G, but diverge from the subtype G viruses previously reported from Russia. GenBank accession numbers U33095-U33096.						
HIV1MLY10A	MLY10A	U33104	1218 bp	env (V1-V5)	Bobkov, A.F.	ARHR 12, 1687 (1996)
Comment: One hundred and thirty subjects living in the Russian Federation were enrolled in this study between 1992 to 1996. Proviral DNA was extracted from PBMCs and the env gene was extended by nested PCR; amplified products were then cloned. The study showed that subtypes B and G are predominant in the Russian Federation, although subtypes A, C, D, and H are also present. In this article special attention is given to two epidemiologically linked patients SHL (U33106-U33108) and MLY (U33104-U33105) whose genetic subtypes could not be identified clearly by the HMA method. SHL became infected through sexual contact with an HIV-1 positive student from Zaire. MLY became infected by a blood transfusion from SHL after a cesarean section in 1987. MLY child is believed to have acquired the disease through breast feeding. The authors concluded that MLY and SHL belonged to the H subtype after phylogenetic tree analysis.						
H92MY14093	92MY14093	U65538	345 bp	env (V3)	Brown, T.M.	ARHR 12, 1655 (1996)
Comment: Blood samples were collected between 1992 and 1993 from 13 IV drug-using prisoners in Kuala Lumpur, Malaysia and one HIV-1 infected baby born in Thailand but adopted by Malaysian parents. PCR products amplified from uncultured PBMCs were directly sequenced. Eleven sequences clustered with the B subtype (U65538-U65548), two grouped in the C subtype (U65549-U65550) and the baby's sequence (U65551) was determined to be subtype E. Subtype C patients were Malaysian nationals who had visited India in 1989 and 1990 for medical treatment. GenBank accession numbers U65538-U65551.						
HIV194UG003	94UG003	U44878	275 bp	env (C2-V3)	Buonaguro, L.	JVI 69, 7971 (1995)
Comment: These 10 sequences are from Gulu, northern Uganda. They are direct sequences of PCR products amplified from uncultured PBMCs. Blood samples were drawn in March 1994 from 217 pregnant women attending a clinic in Gulu, northern Uganda. Ages ranged from 17 to 37 years. The 29 seropositive women (13.4% of the 217 tested) were all asymptomatic. Eight sequences were subtype A and two were D (U44881 U44884). Genbank accession numbers U44878-U44887.						
HIV1U37030	AR06	U37030	331 bp	env (V3)	Campodonico, M.	ARHR 12, 79 (1996)
Comment: Fourteen sequences from a study examining HIV-1 strains in Rosario, Argentina. The cohort included individuals infected through heterosexual and homosexual contact, blood transfusion, and intravenous drug use. The patients were enrolled in the study in April 1995. Two (U37032, U37033) clustered with subtype F sequences, ten (U37030, U37031, U37034-U37042) with subtype B, and one (U37043) appeared to be a B/F hybrid.						

## HIV-1 ENV Sequence Summaries

- HIVU54771 CM240 U54771 9203 bp comp. gen. Carr, J.K. JVI 70, 5935 (1996)  
 Comment: Blood from an asymptomatic heterosexual 21-year-old Thai man was transported from Thailand to the USA where PBMCs were separated and co-cultivated with PHA-stimulated donor PBMCs. DNA from p24 antigen-positive culture was used to amplify the proviral DNA. The complete genomic sequence of the provirus was determined by the compilation of three clones containing different parts of the viral genome. CM240 is an example of a Thai subtype E virus, which is a mosaic of a clade A virus and a clade E virus. GenBank accession number U54771.
- HIVU53278 CMCH1 U53278 287 bp env Cassol, S. ARHR 12, 1435 (1996)  
 Comment: A set of sequences from a study on the detection of HIV-1 subtypes A,B,C, and E in India, Myanmar, Thailand, China, and Indonesia involving dried blood spots collected in 1992. Envelope gene extended by PCR amplification from DNA of dried blood spots. The patients belonged to a wide variety of risk categories. GenBank accession numbers UU53286, U53291 (subtype A); U53304-U53308, U53310, U53311, U53314-U53317( subtype B); U53278-U53285, U53287-U53290, U53292-U53303 (subtype C); U53309, U53312, U53313 (subtype E).
- HIVTW644 TW64-4 U73045 214 bp env (V3) Chang, K.S.S. ARHR In press (1996).  
 Comment: These 16 sequences represent healthy HIV-1 carriers or AIDS patients from Taiwan. Three subtype B sequences in this set were greater than 97% identical to the HXB2/LAI lab strain of HIV-1 (TW83, U73049; TW271, U73059; and TW335, U73061). The manuscript reports that 123 of 143 sequences from Taiwan were subtype B, but only 27 of the 143 sequences were submitted to the sequence databases. Other subtypes found in Taiwan in this study were E (U73060, U73062 and U73070), C (U73055), F (U67765) and G (U73058). GenBank accession numbers for B subtype are U73045–U73054, U73056, U73057, U73059, U73061 and U73063–U73069.
- HIVU50207 Z321B U50207 1497 bp env Choi, D.J. ARHR In press (1996)  
 Comment: The virus HIVZ321B is a later passage of HIVZ321, which was isolated from a 1976 Zairian serum sample (GenBank accession number M15896). Z321 was grown to industrial scale in a chronically infected T-cell line to manufacture an inactivated, therapeutic HIV-1 immunogen. Z321B contains a mutation in the termination codon of the tat gene and extends further downstream by 48 nucleotides. The authors present evidence for Z321 being an A/G recombinant. GenBank accession numbers U50207 and U50208.
- HIV1GP41 BSMADGP41 X83215 372 bp gp41 Cohen, H.J.M. Lancet 345, 856 (1996)  
 Comment: One of two partial env group O sequences, one of gp41 and the other of gp120. GenBank accession numbers X83215 and X83216.
- HIV1U56263 2BD20 U56263 656 bp env (C2-V5) Contag, C.H. Unpublished (1996)  
 Comment: These sequences come from a study of mother to child transmission of HIV1 in Sweden involving five subtypes. Subtype A: mother 4, and infant 4 (U56274-U56283, U56328); Subtype B: mother 2, infant 2, mother 6, and infant 6 (U56263-U56273, U56288-U56291, U56299, U56300, U56303, U56317-U56321, U56335); Subtype C, mother 5, infant 5, mother 7, and infant 7; Subtype D, mother 3, infant 3 (U56304-U56306, U56310-U56312, U56330); Subtype E, mother 1, infant 1 (U56309, U56329). Proviral DNA derived from PBMCs or plasma.
- HIVG134 G134 X90912 873 bp env (V3-V5) Delaporte, E. AIDS 10, 903 (1996)  
 Comment: In this study, 17 partial HIV-1 env (V3-V5) gene sequences were determined from 17 different patients selected from a study involving serological screening of 7,082 patients in Libreville, Gabon, and 771 pregnant women and 886 asymptomatic adults in Franceville, Gabon. The study took place from 1986-1994 during which the prevalence of HIV infection in Gabon was low (0.7 - 1.6% in pregnant women, 2.1 - 2.6% in the general population) and remained stable. The 17 isolates sequenced represented five different subtypes (A, C, D, F, and G) and Group O. The high sequence diversity, and low prevalence rates are similar to Cameroon, but different from the rest of Africa. Of the 17 strains, 10 were isolated from Libreville. Of these, 4 were from asymptomatic seropositive persons in 1988 and 6 were collected from AIDS patients between 1989 and 1993. The remaining 7 were collected between 1988 and 1989 from AIDS patients in Franceville. GenBank accession numbers X90912 (G134), X90913 (LBV10-5), X90914 (LBV2-3), X90915 (G135), X90916 (G98), X90917 (G41), X90918 (LBV23-10), X90919 (G109), X90920 (G141), X90921 (VI1076), X90922 (VI526), X90923 (VI354), X90924 (VI685), X96526 (VI686), U09665 (LBV21-7), L22953 and U09665 (VI525). Isolate G139 is not available from GenBank.
- HIVU43035 U43035 235 bp env (V3) Diaz, R. Unpublished (1996)  
 Comment: Set of 124 closely related sequences presumably belonging to subtype B. All 124 sequences came from patients from the United States who had been infected by a common source. GenBank accession numbers U29433-U29437, U29956-U30054, and U43035-U43054. Gag sequences from 12 clones are also available in GenBank entries U31573-U31584.

## HIV-1 ENV Sequence Summaries

HIVU43986 D1-116 U42986 240 bp env (C2-V3-C3) Diaz, R. ARHR 12, 1291 (1996)

Comment: These sequences come from a study on the lack of dual HIV infection in a transfusion recipient who was exposed to two seropositive blood components. The patient was a 54-year-old male with oat cell carcinoma of the lung who was treated with prednisone at the time of index transfusion. He was transfused in November 1984. Samples of sera and leukocytes from both donors and from the dual recipient were analyzed. GenBank accession numbers U43986-U44023.

HIVU51942 U51942 325 bp env (C2V3-C3) Diaz, R. Unpublished (1996)

Comment: This work also includes a gag sequence. GenBank accession numbers U51942, U52055-U52063 and U52194.

HIV1V3NO1 NO1 X92902 252 bp env (V3) Engelstad, M. ARHR 12,1733 (1996)

Comment: Sequences of 40 individuals of Norwegian origin from four major risk groups. Eleven were homosexual or bisexual men, 11 were IVDUs, 4 were heterosexual partners of IVDUs, 6 were hemophiliacs who had received contaminated blood products, and 8 were heterosexual individuals infected through intercourse with persons from Zambia (3), USA (1), Grenada (1), Italy (2), and South Africa (1). The dates of seroconversion were unknown. Thirty-eight of the patients were asymptomatic and two of the hemophiliacs were classified as CDC IV at the time when the samples were obtained. Thirty-six of these sequences are subtype B (X92902-X92912, X92915, X92916, X92919-X92941) and four are subtype C (X92913, X92914, X92917, X92918). GenBank accession numbers X92902-X92941.

HIVU56866 C499env1 U56866 573 bp env Fultz, P.N. Unpublished (1996)

Comment: A set of 12 env sequences from a study on the diversification of two HIV-1 LAI Subtype B strains during the dual infection of a chimpanzee for 9 years. GenBank accession numbers U56866-U56887. Also, see GenBank accession numbers U56888-U56899 for gag sequences from the same study.

HIVU51188 90CR402 U51188 9843 bp comp. gen. Gao, F. JVI 70, 7013 (1996)

Comment: One of a set of three complete genomes from a study linking the HIV-1 epidemic in the heterosexual population in Thailand to an A/E recombinant. 90CR402, previously named CAR-E 4002, was obtained from a man from Bangui, Central African Republic, who had lymphadeopathy, diarrhea, severe weight loss and recurrent respiratory infections. He was infected through heterosexual contact, but the year of infection is unknown. 90CR402 (U51188) was first adapted to growth in chimpanzee cells, expanded in chimpanzee cells, and then re-expanded in human PBMCs before lambda cloning and sequencing. 93TH253 (U51189) is from a 21-year-old man from Chiang Mai, Thailand and was previously named CMU010 or 302053. The patient had end-stage AIDS. The mode and year of infection are unknown. 93TH253 was isolated and expanded in human PBMCs, then expanded in H9 cells followed by lambda cloning and sequencing. 92UG037 (U51190) was obtained from WHO-NIAIDS and comes from an asymptomatic 31-year-old female from Entebbe, Uganda, early in infection. The year of infection is unknown and the mode of infection was heterosexual contact. 92UG037 was established and propagated by cocultivation with normal donor lymphocytes, and then PCR amplified and sequenced. 93TH253 and 90CR402 are subtype E (A/E recombinant). Comparison of the two strains showed that they were derived from a common A/E recombinant ancestor, presumably from Central Africa. 92UG037 is subtype A. LTR sequences are available under accession numbers U51282-U51297.

HIVUGO2116 UGO2116 U27426 2928 bp env Gao, F.J. JVI 70, 1651 (1996)

Comment: The complete gp160 coding region of this isolate was sequenced along with those of others collected at major epicenters of the AIDS epidemic during a study by Gao et al. The 35 members of this representative panel include members of all major sequence subtypes of HIV-1 group M (clades A-G) as well as an inter-subtype recombinant (F/B) from an infected individual in Brazil. In this panel, all subtype E and three subtype G viruses initially classified on the basis of partial env sequences were found to cluster in subtype A in the 3' half of their gp41 coding region, suggesting that they are also recombinant. The biological activity of PCR derived envelope genes was examined in a single round virus infectivity assay. This analysis identified 20 clones, including one from each subtype or recombinant, that expressed fully functional envelope glycoproteins. GenBank accession numbers U27443-U27445, U27434, U27426, U27419, U27413, U27408, U27401, U27399, U04900-U04929, U30312, U43386, L34667, U08797, U08794, U09131, U08801, U08441-U08447, U09127, U09126.

HIVU48855 94CU053 U48855 1416 bp env (V3) Gomez, C.E. ARHR 12, 553 (1996)

Comment: DNA sequence of the gp120 cds of a HIV-1 isolate from a bisexual male, most probably infected in Cuba in 1992 by heterosexual contact. The virus was isolated two years after seroconversion by cocultivation of patient PBMCs with seronegative donor PBMCs. Nested PCR was used to amplify the gp120 gene and the C2-V3 region. Five clones from the C2-V3 region were isolated and studied. The amino acid sequence GRGR in the tip of the V3 loop is reported here for the first time. This atypical sequence suggests that this virus can escape from antibodies directed against the V3 region of other HIV-1 isolates more frequently found in America. The sequence clustered with subtype B sequences SF2 and LAI. GenBank accession number U48855.



SIVCPZANT CPZANT U42720 8182 bp comp. gen. Vanden Haesevelde, M. Virology 221, 346 (1996)

Comment: A simian immunodeficiency virus phylogenetically linked to HIV-1 which was isolated from a captured wild chimpanzee from Zaire. This is the third SIV strain linked to HIV-1 after SIVCPZ-GAB (X52154) and SIVCPZ-GAB2 (U11495) isolated from chimps in Gabon. While SIVCPZ-ANT and SIVCPZ-GAB share a common ancestor with HIV-1, they differ in that the SIVCPZ strains have highly conserved V3 regions and HIV-1 has a highly variable V3 region. SIVCPZ-ANT is considered to be an outgroup of HIV-1 and is used to suggest the possibility of various introductions of HIV-1 into the human population.

HIVBJ1 BJ1 U61854 255 bp env (V3) Heyndrickx, L. ARHR 12, 1495 (1996)

Comment: These 18 sequences are from female prostitutes, born in either Ghana or Togo, who live in Benin. Fifteen are from directly sequenced PCR products, derived via RT-PCR from patient serum RNA. Three (233, 251 and 253) are from cloned PCR products, also by RT-PCR from serum RNA. Another subtype A sequence (366, U61870) is not included here, because it was nearly identical (254 of 255 bases identical) to the SF170 sequence from 1988, and thus it likely represents a lab artifact. GenBank accession numbers U61854–U61869, U61871 and U61873.

HIVU63314 HIV-1MN U63314 275 bp env Hua, J. Virology In press (1996)

Comment: HIV-1 MN env and rev gene sequences from a study on the changes of function resulting from a natural sequence variation in the activation domain of HIV-1 rev. MN is from the USA. GenBank accession number U63314.

HIVU47562 A1-E1 U47562 608 bp env Hutto, C.J. JVI 70, 3589 (1996)

Comment: These sequences come from a study on twins with different disease courses. Envelope gene was extended by nested PCR amplification from proviral DNA derived from patients PBMCs. Heterozygotic twins who had been perinatally infected were observed during their first 2 years of life. Twin A (U47562-U47572), the first born, remained asymptomatic while twin B (U47573-U47588) developed AIDS when he was 6 months old and died when he was 22 months old. The absence of neutralizing antibodies may correlate with disease progression since twin A developed neutralizing antibodies and twin B did not. The samples were determined to be nonsyncytium inducing and subtype B. Also see GenBank accession numbers U47589-U47613 for tat sequences from the same patient.

HIVMCK1 MCK1 D86068 9752 bp comp. gen. Iwatani, Y. Unpublished (1996)

Comment: This sequence is ~98% identical to HXB2 and other IIB lab strains of HIV-1. PM213 is another complete genome also ~98% identical to HXB2. GenBank accession numbers D86068 and D86069.

HIV1686EN VI686 X96526 2640 bp env Janssens, W. AIDS 10, 903 (1996)

Comment: A group O sequence from a study on the characterization of HIV-1 group O viruses. This sequence is from a 1992 sample taken from a Gabonese woman with AIDS (Libreville). The Method of DNA isolation was not described. DNA was PCR amplified and cloned. See also GenBank accession numbers X90912-X90924.

HIVV3REO1 1A-2 D78614 105 bp env (V3) Kakizawa, J. ARHR 12, 561 (1996)

Comment: These sequences come from a study of the diversity of the HIV1 env V3 region in saliva. Eight saliva samples were collected from seven patients. Two were asymptomatic carriers (isolates 7 and 8), three had AIDS-related complex (isolates 2, 4, 5, and 6, 5 and 6 being from the same patient), and two were patients with AIDS (isolates 1 and 3). Saliva samples corresponding to isolates 1 through 5 were collected between April and June, and isolates 6 through 8 were collected in January 1995. Five cases were children with hemophilia (isolates 1-4, 6 and 7) and two patients were homosexual adults (isolates 5 and 8). Proviral DNA was extracted by glass powder method. DNA was then PCR amplified and sequences. GenBank accession numbers: Isolate 1, D78614-D78616; Isolate 2, D78617; Isolate 3, D78618-D78621; Isolate 4, D78622-D78623; Isolate 5, D78624-D78626; Isolate 6, D78627-D78630; Isolate 7, D78631-D78633; Isolate 8, D78634-D78637. These sequences belong to subtype B and, of the previously-reported Japanese strains, are more closely related to SF162 than to MN.

HIVH13958 H13958 L07243 330 bp env (V3) Kalish, M. Unpublished (1996)

Comment: Twenty-five Haitian sequences were PCR amplified from PBMCs. The set includes direct sequences of PCR amplification products, consensus sequences of multiple clones of PCR products plus one direct sequence, and single clones of PCR products. Full length env for some of these have been expressed. All sequences clustered with subtype B. GenBank accession numbers L07145–L07161, L07163–L07165, L07167–L07207, L07209–L07239, L07241–L07246, U08441–U08447.

HIV074CDE 074CDE Z75958 276 bp env (V3) Kampinga, G.A. Unpublished (1996)

Comment: Three hundred and twelve sequences of Rwandan women and their offspring, taken from seven infants and three mothers. Mother 566 was apparently infected with subtype A and subtype C HIV-1. All other sequences are subtype A. GenBank accession numbers for child 566 are Z76160–Z76161, Z76167–Z76168, Z76169–Z76176, Z76233–Z76248, Z76262–Z76273 and Z76717–Z76724; mother 730, Z76353–Z76362; child 564, Z76074–Z76083; mother 226, Z76046; child 538, Z76134–Z76143, Z76373–Z76382, Z76393–Z76412; child 074, Z75958; child 082, Z75998–Z76009, Z76650; child 081, Z75959–Z75968; child 618, Z76198–Z76207; mother 439, Z76048–Z76057, Z76064–Z76068 and Z76070.

## HIV-1 ENV Sequence Summaries

HIVJGV10 4664 Z68508 276 bp env (V3) Kuiken, C.L. J.Gen. Virol. 77, 783 (1996)

Comment: These subtype B sequences are from a set containing 15 Dutch homosexuals, 19 Dutch intravenous drug users, 2 German homosexuals, 2 German intravenous drug users, 5 Scottish homosexuals and six Scottish intravenous drug users. The sequences were used in a study of HIV-1 Vpr, Vpu, and V3 regions and how they vary between risk groups. GenBank accession numbers Z68687-Z68693 and Z68508-Z68616.

HIVH0001L H0001L Z67875 270 bp env (V3) Kuiken, L. AIDS In press (1996)

Comment: These subtype B sequences come from a study on the limited intra-subject evolution of the envelope V3 region in the Amsterdam population. Taken from a cohort of homosexual men who seroconverted between 1985 and 1989, these sequences are from direct sequencing of PCR products after RT-PCR from serum DNM. GenBank accession numbers Z67875, Z67876, Z68110, Z68109, Z68015-Z68089, Z67885-Z67960.

HIVU58393 1P74E001 U58393 252 bp env (V3) Leigh-Brown, A.J. Unpublished (1996)

Comment: A set of 73 env sequences from a Scottish study on the variability of env and pol genes in HIV-1 LAI during zidovudine therapy. PCR amplified PBMC DNA were sequenced and are most probably sybtype B. GenBank accession numbers U58393-U58465.

HIVU68496 sample 136 p1 U68496 276 bp env (V3) Leitner, T. PNAS 93, 10864 (1996)

Comment: This set of 26 sequences from 13 samples contains sequences from env V3 and gag p17. The set is derived from an exactly known Swedish transmission history and includes serial samples from some patients. The index case (patient 1) was a Swedish male who is believed to have contracted HIV while visiting Haiti in 1980. Six Swedish females (patients p2, p4, p5, p7, p8, and p11) were infected by patient 1. Two males (patients p6 and p10) were then infected by these females, and two HIV-infected children (patients p3 and p9) were born to the women. The phylogeny of this data set spans the time 1980 to 1994. GenBank accession numbers p1, U68496, U68497, U68509; p2, U68498, U68511; p3, U68499, U68500, U68512, U68513; p5, U68501, U68514; p6, U68502, U68515; p7, U68503, U68516; p8, U68504, U68505, U68517, U68518; p9, U68506, U68519; p11, U68507, U68508, U68520, U68521. Sequences are unavailable for p4 and p10.

HIVU69646 RU3 U69646 258 bp env (V3) Leitner, T. ARHR 12, 1595 (1996)

Comment: This set contains 22 env V3 sequences from Russian infected patients. The set contains both epidemiologically linked and unlinked patient sequences. Subtypes A, B, F, and G were found from hetero-, homo-, and bisexual as well as nosocomially infected patients. All sequences are direct population estimates from uncultured patient PBMCs and were characterized on MT-2, CEM, and Jurkat-tat cells. GenBank accession numbers U69646-U69667.

HIV1U56146 14Pb1-16 U56146 629 bp env (V3-V5) Liu, S-L. Unpublished (1996)

Comment: Set of sequences from a study on different patterns of progression to AIDS from the same source of infection. GenBank accession numbers U56146-U56235.

HIVU54646 3BC01V2 U54646 174 bp env (V1/V2) Lockey, T.D. ARHR 12, 1297 (1996)

Comment: These sequences represent 22 clones from 2 descendant HTLV-IIIb cultures. The HTLV-IIIb stocks were propagated on H9 cells. DNA was isolated and PCR used to amplify the envelope gene. The sequences were then compared to each other, and to other previously isolated clones, to determine the degree of heterogeneity. The heterogeneity found poses questions about the validity of comparing results from different labs. GenBank accession numbers U54646-U54689.

HIVU57104 e01 U57104 360 bp env (C2-V3) Lorenzo, E. Unpublished (1996)

Comment: A set of 113 env sequences and 88 tat sequences from U.S. patients derived from a study on the variability of tat and env genes in HIV-1. Sequences are subtype B. GenBank accession numbers U57104-U57216 and U57217-U57304 for the tat sequences.

HRW890388 RR890388 L76870 270 bp env (V3) Lukashov, V.V. ARHR 12, 951 (1996)

Comment: These sequences are from recent immigrants to the Netherlands from various countries where AIDS is endemic. Unconventional country codes were used in the common names. Viral RNA was prepared from patient serum and RT-PCR was used to amplify the V3 region of the env gene. The PCR products were directly sequenced. Individuals originating from African countries belonged to subtypes A, C, and D. Individuals originally from Zaire showed subtypes F and G. GenBank accession numbers L76870-L76913 and L86887.

HIVIENVAA 131871 L76842 270 bp env (V3) Lukashov, V.V. ARHR 12, 1179 (1996)

Comment: This set of sequences comes from a study that links the origin of the AIDS epidemic in Northern Europe to the United States. HIV1 RNA coding for the V3 envelope region was derived from serum samples taken at seroconversion from 31 homosexual men who seroconverted in 1985-1988 and 12 IVDUs who seroconverted in 1986-1990 in Amsterdam, and 11 IVDUs from Baltimore who seroconverted in 1988-1990. In addition, V3 sequences from 8 IVDUs in Scotland and Germany and 10 homosexual men in Scotland, Germany, the United States, and Russia were used to conclude the existence of a link to the US in the origin of the northern European AIDS epidemic. GenBank accession numbers L76842-L76863.

- HIVU48274 1018 U48274 644 bp env (C2-V5) McCutchan, F.E. JVI 70, 3331 (1996)  
Comment: Four of these sequences are from Uruguayan servicemen who acquired HIV-1 infections while deployed as United Nations peacekeepers in Cambodia in 1993. Two sequences are from samples collected in 1993 in Thailand. One sequence is from a U.S. serviceman who acquired an HIV-1 infection while deployed in Thailand. All of these patients were asymptomatic when samples were collected. Six sequences were from patients hospitalized with AIDS-related illnesses in northern Thailand. Viral DNA was PCR amplified from patient PBMCs. All sequences are HIV-1 clade E. GenBank accession numbers U48272-U48278 and U48264-U48269.
- HIVU57788 KI4803 U57788 1610 bp env McKeating, J.A. Virology 220, 450 (1996)  
Comment: HXB2 viruses chimeric for gp120 were constructed from a primary isolate. The primary isolate was KI4803 which comes from Sweden and whose subtype is uncertain. Primary and chimeric viruses were compared to ascertain differences in functionality. XHB2 chimeras showed same patterns of cell tropism and cytopathicity. Both primary and chimeric viruses were sensitive to neutralization by sCD4 and had the same gp120 conformation. GenBank accession numbers U57788-U57794.
- HAR20016 AR20016 U68522 258 bp env (V3) Marquina, S. ARHR 12, 1651 (1996)  
Comment: Blood samples from four unrelated patients in Buenos Aires, Argentina, were collected in 1993. Two patients had AIDS: one was an intravenous drug user, 21280 (U68524), and the other a promiscuous heterosexual, 21281 (U68525). Two samples came from asymptomatic patients, 20021 (U68523) and 20016 (U68522). Direct sequencing of PCR products was done from uncultured PBMCs. Two sequences were of subtype F (21280 and 20016) and one of subtype B (21281). The last sequence (20021) was a B/F recombinant.
- HESP11158 ESP1-1158 U62618 402 bp env Mas, A. ARHR 12, 1647 (1996)  
Comment: These sequences come from blood samples taken from a 35-year-old man from Spain collected in April and September 1995. The V3 region was PCR amplified from uncultured PBMCs, cloned into PGEM-SZF, and an individual clone sequenced. The sequences belong to group O. The April sequence has GenBank accession number U62618 and the September sequence has number U62617.
- HIVU66414 UY726 U66414 313 bp env Medina, R.D. ARHR 12, 1491 (1996)  
Comment: These nine subtype B sequences were derived from blood samples obtained in March-April 1995 from nine HIV-1 infected patients in Montevideo, Uruguay. Uncultured PBMCs were lysed and viral DNA was amplified by nested PCR. These sequences show a high degree of heterogeneity in the apex motif of V3. GenBank accession numbers U66414-U66422.
- HIV1U29209 HCM9 U29209 219 bp env Menu, E. Unpublished (1995).  
Comment: This subtype B sequence is from Ho Chi Minh city, from a woman infected by her HIV seropositive sexual partner who was thought to have been infected while traveling in Europe, Genbank accession number U29209. Three other sequences in this Vietnamese study from IV drug users in Ho Chi Minh city and Dong Nai, and a female prostitute in Can Tho were found to be subtype E. Genbank accession numbers U29206-U29209
- HIV1HWCL1 HWCL1 U34049 487 bp env (V3) Montpetit, M. ARHR 11, 1421 (1995)  
Comment: This sequence is the first published sequence of subtype A HIV-1 in Canada. The patient had moved from Uganda in 1983, and was diagnosed as HIV+ in 1989. Viral RNA was recovered from archived, stored patient serum by binding viral particles to CD4-coated wells of an ELISA plate. After RT-PCR, products were cloned and 10 clones were sequenced. This sequence is from a single clone, L1.
- HIVU48719 HIV1VN4 U48719 322 bp env (V3) Nerurkar, V.R. ARHR 12, 841 (1996)  
Comment: A genotypic analysis from IDUs and CSWs in Vietnam to determine if concurrent epidemics with different HIV-1 subtypes are occurring among the high risk-behavior groups. Blood samples were collected from two HIV-1 CSWs and three IDUs in southern Vietnam during April and May 1995. VN1 (U45239) and VN2 (U45240) were from healthy 17 and 25 year-old female prostitutes from Can Tho and An Giang. VN3 (U48720) and VN4 (U48719) were a 43 year-old male IV drug user with pruritus and splenomegaly from Nha Thang and a 31 year-old healthy IV drug user male from Nha Thang respectively. Genomic DNA was extracted. The V3 loop region was then amplified through PCR and sequenced. It was determined that the Vietnam HIV-1 strains belong to subtype E and that the patients had been infected with indigenous strains circulating within Vietnam.
- HIVU67348 VI1011 U67348 453 bp env Nyambi, P.N. ARHR In press (1996)  
Comment: Five HIV-2 sequences derived for use in an examination of the cross-neutralization characteristics between HIV-1 and SIVcpz and those between HIV-1 and HIV-2. Nyambi et al. found that the cross-neutralization between HIV-1 and HIV-2 was less extensive than between the HIV-1 and SIVcpz. In addition they saw that, though their binding capacity did not readily reflect their neutralizing capacity, a majority of HIV-1 and SIVcpz sera bound to the V3 peptides while the HIV-2 sera lacked the neutralizing antibodies to the homologous isolate and did not have any reactivity to the V3 peptide. GenBank U67348-U67352.

## HIV-1 ENV Sequence Summaries

- HIV1U52247 P1T1A1 U52247 243 bp env (V1-V2) Palmer, C. Virology 220, 436 (1996)  
 Comment: Variations in the V1V2 region were followed over time in six HIV1 infected individuals. Peripheral blood samples were obtained from six seropositive males (CDC II) attending an STD clinic. The V1V2 sequences were cloned into HXB2 to produce chimeras. The chimeras showed that the V1V2 region of gp120 can determine both tropism and cytopathicity independently from the V3 region. GenBank accession numbers for patient 1, U52247-U52264; patient 2, U52265-U52285; patient 3, U52286-U52303; patient 4, U52304-U52315; patient 5, U52316-U52333; patient 6, U52334-U52339.
- HIV1ES106 ES106 U40533 402 bp env (C2-V3) Quinones, M.E. ARHR 12, 955 (1996)  
 Comment: These subtype B sequences are from 41 patients sampled in Madrid, Spain between 1985 and 1991. Proviral DNA was extracted from uncultured patient PBMCs and the C2V3 region was PCR amplified. The PCR products were directly sequenced. Two of the sequences reported in this set (D22-28 and D22-48) were 99.5% identical to the LAI strain of HIV-1. Three other groups of sequences had members that were greater than 98% identical to each other (R1, R2 and R3; THF13-2, THF12-24; S1, S4). GenBank accession numbers U40533-U40552 and U45286-U45307.
- HIVENVB HIV1BB L78831 1546 bp env Ray, S.C. Unpublished (1996)  
 Comment: These subtype B sequences come from a study on the cytolytic T lymphocyte strain-specific responses that are directed against the HIV-1 env. Virus was isolated from PBMCs. GenBank accession numbers L78831 and L78832.
- HIVKZ21 KZ21 U43097 945 bp partial env Reitz, M. Unpublished (1990)  
 Comment: These subtype A sequences are from Zaire. GenBank accession numbers U43097-U43100.
- HIV1U61875 94TZ1574 U61875 342 bp env (C2V3) Robbins, K.E. ARHR 12, 1389 (1996)  
 Comment: These sequences come from a study on the genetic variability of HIV1 in rural Northwest Tanzania. Sequences were obtained by PCR amplification of patient PBMCs. Seven of the Tanzanians lived in the Mara region and their samples were collected in 1994. The other patient, 87TZ4622, was originally from the Mara region, but had lived in Kigoma for several years. The specimen used was collected in 1987. Sequences 94TZ1627, 87TZ4622, 94TZ1585, and 94TZ1604 are subtype D. Sequences 94TZ1577, 94TZ1576, 94TZ1574, and 94TZ1584 are subtype A. GenBank accession numbers U61875-U61881 and U65075.
- HIV1U31585 SP203 U31585 648 bp env (V3) Sabino, E.C. AIDS 10, 1579 (1996)  
 Comment: This is a set of 11 sequences from a study on the prevalence of HIV-1 subtypes in Sao Paulo, Brazil. Five sequences are subtype B (U31586, U31587, U31589-U31591), one sequence is subtype C (U31585), and four sequences are subtype F (U31588, U31592-U31595).
- HIVETH2220 ETH2220 U46016 9031 bp comp. gen. Salminen, M.O. ARHR 12, 1329 (1996)  
 Comment: U46016 is the first reported (almost full length) subtype C sequence from Ethiopia. In its genomic organization, this clone closely resembles subtype A, B, and D isolates except that the core promoter contains three potential binding sites for the transcription factor NF-kB instead of containing two.
- HIV1G1X11 G1-11 Z50841 105 bp env (V3) Schreiber, M.G. Unpublished (1996)  
 Comment: Sequences from a study of the loss of antibodies specific for the V3 domain over time in certain HIV-1 variants. Proviral DNA extracted from patients PBMCs. Probably subtype B. GenBank accession numbers Z50841-Z50847.
- HIVU45860 1018674A U45860 280 bp env (C2V3) Schwartz, D.H. Unpublished (1996)  
 Comment: These subtype B sequences are from a study of the envelope glycoprotein C2-V3 region on isolates obtained from PBMCs of four HIV-1 infected patients. GenBank accession numbers for patient 101867 are U45860-U45876, U49624-U49640; patient 10188B, U51311-U51326; patient 10185W, U49600-U49623; patient 10187Y, U49518-U49553.
- HIVU45330 U45330 363 bp env (V3) Sheehy, N. J.Gen.Virol 77, 1071 (1996)  
 Comment: Set of subtype B sequences from an AIDS patient from the United Kingdom who had received treatment with zidovudine for 9 months. Proviral DNA obtained from PBMCs drawn 13 months and 10 months prior to death and from autopsy samples of cardiac blood, lymph node, spleen, bone marrow and brain was PCR amplified and sequenced. A reduction in genetic heterogeneity of the envelope region of viruses present in the proviral blood population occurred during treatment coinciding with increased pol heterogeneity. GenBank accession numbers U45330-U45421.
- HIV1U29179 UIND1 U29179 1488 bp env Tripathy, S.P. ARHR 12, 1199 (1996)  
 Comment: Part of a set of nine sequences from New Delhi and Pune, India, eight of which were subtype C (U29179, U29694-U29698, U31362-U31363) and one of which was subtype B (U31364). All 8 subtype C sequences were from heterosexually infected patients. DNA was isolated from cocultured PBMCs after one week of culture. PCR product was cloned and a single clone was sequenced.

## HIV-1 ENV Sequence Summaries

SIVmac251 SIU62333 U62333 1114 bp env Trivedi, P. JVI 70, 6875 (1996)  
 Comment: Fifty-one env sequences from a study of intrarectal transmission of SIV in rhesus macaque monkeys. Trivedi et al. found that a condition now called transient viremia sometimes occurs after mucosal inoculation of monkeys with low doses of SIV as opposed to the more prevalent persistent infection with evident disease progression. Also, after a 1000 infective dose, they found that transiently viremic monkeys were resistant to an intrarectal SIVmac challenge but not to an intravenous SIVmac challenge. GenBank U62333-U62383.

HIVFF1 FF1 Z76463 303 bp env (V3) van der Hoek, L. J. Gen. Virol. In press (1996)  
 Comment: These subtype B sequences are of 81 clones (patient N) and 105 clones (patient F) from serum, sigmoid tissue and fecal matter from each patient. All sequences from patient N were more similar to other sequences from patient N than to any other sequence in the database. Likewise all sequences from patient F were most similar to other patient F sequences. Both patients are from the Netherlands. GenBank accession numbers Z76463–Z76648.

HIVIU60152 ID4-77c7 U60152 939 bp env Wang, W.K. ARHR 12, 1195 (1996)  
 Comment: This study concentrates on the change of cysteine residues in region 1 of gp120 HIV-1 Subtype B. Sequential isolates from eight subjects were used though these 11 sequences account for only one of the subjects. Subjects came from a group of 315 homosexual and bisexual men who have been followed at the Fenway Community Health Center in Boston and were enrolled between January 1985 and June 1986. Viruses were isolated from PBMCs of the subjects by co-cultivation with PBMCs of HIV-1 seronegative donors. GenBank accession numbers U60152-U60162.

HIVBJP23A BJP23 D67089 264 bp env (C2V3) Xin, K. Lancet 346, 1372 (1996)  
 Comment: This pair of sequences is from a study of a dual infection with HIV1 Thai subtype B and E. D67089 is Subtype E and D67090 is Subtype B or a B/E recombinant. GenBank accession numbers D67089 and D67090.

HIVU32658 NA111 U32658 285 bp env (V3) Zachar, V. ARHR 12, 75 (1996)  
 Comment: This was a May-June 1992 study of pregnant women from the Pumwani Maternity Hospital in Nairobi, Kenya. Viral RNA was concentrated from patient serum just prior to delivery, and the envelope C2-V3 region was amplified by RT-PCR. The PCR product was cloned and 20 clones from each patient were sequenced. Patients from this study had viral subtypes A (U32658, U33763, U33764, U33766, U33767, and U34905), C (U33762), and D (U33765).

HIVU53192 BTS11 U53192 285 bp env (V3) Zachar, V. ARHR 12, 1069 (1996)  
 Comment: Genetic analysis of the V3 env region of virus isolates obtained in 1993 from 11 homosexual men living in the inner city of Bratislava. A 32-year-old homosexual man from Prague was also included in the study. Viruses were cultivated in PBMCs. The C2V3 region of HIV-1 LAI was amplified by nested PCR. PCR product was cloned and eight clones from each patient were sequenced. These strains cluster in the B clade together with the majority of North American and western European strains. GenBank accession numbers U53192-U53203.

HIVU50780 AD39PB1 U50780 1047 bp env (V1-V5) Zhu, T. JVI 70, 3098 (1996)  
 Comment: DNA extracted from PBMCs of an acute seroconverter male patient, AD39, who was infected with HIV-1 through homosexual transmission by his partner AD38. Sequences spanned by primers PE1 and P2 from the gp120 gene were expanded by PCR amplification. A second round of PCR amplification expanded V1-V2 sequences (using inner primers P1 and P10) and V3 (using inner primers P5 and PV3). AD39PB1 has been characterized as non-syncytium inducing (NSI). GenBank accession numbers U50780-U50815.

## HIV-1 NEF Sequence Summaries

LOCUS	COMMON	ACCESSION	LENGTH	REGION	FIRST AUTHOR	REFERENCE
HIVU48901	122-16	U48901	615 bp	nef	Artenstein, A.W.	ARHR 12, 557 (1996)
Comment: Sequences derived from PCR amplified PBMC DNA from nineteen Thai individuals. Only two clones (28-19, 28-2) from one subject clustered with subtype B sequences while the rest clustered with subtype E sequences. The lack of subtype E nef sequences led Artenstein et al. to begin this study. GenBank accession numbers U48897-U48934.						
HIVU54771	CM240	U54771	9203 bp	comp. gen.	Carr, J.K.	JVI 70, 5935 (1996)
Comment: Blood from an asymptomatic heterosexual 21-year-old Thai man was transported from Thailand to the USA where PBMCs were separated and co-cultivated with PHA-stimulated donor PBMCs. DNA from p24 antigen-positive culture was used to amplify the proviral DNA. The complete genomic sequence of the provirus was determined by the compilation of three clones containing different parts of the viral genome. CM240 is an example of a Thai subtype E virus, which is a mosaic of a clade A virus and a clade E virus. GenBank accession number U54771.						
HIVU51188	90CR402	U51188	9843 bp	comp. gen.	Gao, F.	JVI 70, 7013 (1996)
Comment: One of a set of three complete genomes from a study linking the HIV-1 epidemic in the heterosexual population in Thailand to an A/E recombinant. 90CR402, previously named CAR-E 4002, was obtained from a man from Bangui, Central African Republic, who had lymphadenopathy, diarrhea, severe weight loss and recurrent respiratory infections. He was infected through heterosexual contact, but the year of infection is unknown. 90CR402 (U51188) was first adapted to growth in chimpanzee cells, expanded in chimpanzee cells, and then re-expanded in human PBMCs before lambda cloning and sequencing. 93TH253 (U51189) is from a 21-year-old man from Chiang Mai, Thailand and was previously named CMU010 or 302053. The patient had end-stage AIDS. The mode and year of infection are unknown. 93TH253 was isolated and expanded in human PBMCs, then expanded in H9 cells followed by lambda cloning and sequencing. 92UG037 (U51190) was obtained from WHO-NIAIDS and comes from an asymptomatic 31-year-old female from Entebbe, Uganda, early in infection. The year of infection is unknown and the mode of infection was heterosexual contact. 92UG037 was established and propagated by cocultivation with normal donor lymphocytes, and then PCR amplified and sequenced. 93TH253 and 90CR402 are subtype E (A/E recombinant). Comparison of the two strains showed that they were derived from a common A/E recombinant ancestor, presumably from Central Africa. 92UG037 is subtype A. LTR sequences are available under accession numbers U51282-U51297.						
SIVCPZANT	CPZANT	U42720	8182 bp	comp. gen.	Vanden Haesevelde, M.	Virology 221, 346 (1996)
Comment: A simian immunodeficiency virus phylogenetically linked to HIV-1 which was isolated from a captured wild chimpanzee from Zaire. This is the third SIV strain linked to HIV-1 after SIVCPZ-GAB (X52154) and SIVCPZ-GAB2 (U11495) isolated from chimps in Gabon. While SIVCPZ-ANT and SIVCPZ-GAB share a common ancestor with HIV-1, they differ in that the SIVCPZ strains have highly conserved V3 regions and HIV-1 has a highly variable V3 region. SIVCPZ-ANT is considered to be an outgroup of HIV-1 and is used to suggest the possibility of various introductions of HIV-1 into the human population.						
HIVMCK1	MCK1	D86068	9752 bp	comp. gen.	Iwatani, Y.	Unpublished (1996)
Comment: This sequence is ~98% identical to HXB2 and other IIB lab strains of HIV-1. PM213 is another complete genome also ~98% identical to HXB2. GenBank accession numbers D86068 and D86069.						
HIVU61773	And1.dat	U61773	618 bp	nef	Mariani, R.	Unpublished (1996)
Comment: Set of 62 sequences from a German study on the frequency of defective nef alleles in an HIV-1 long term survivor. GenBank accession numbers U61773-U61834.						
HIVETH2220	ETH2220	U46016	9031 bp	comp. gen.	Salminen, M.O.	ARHR 12, 1329 (1996)
Comment: U46016 is the first reported (almost full length) subtype C sequence from Ethiopia. In its genomic organization, this clone closely resembles subtype A, B, and D isolates except that the core promoter contains three potential binding sites for the transcription factor NF-kB instead of containing two.						